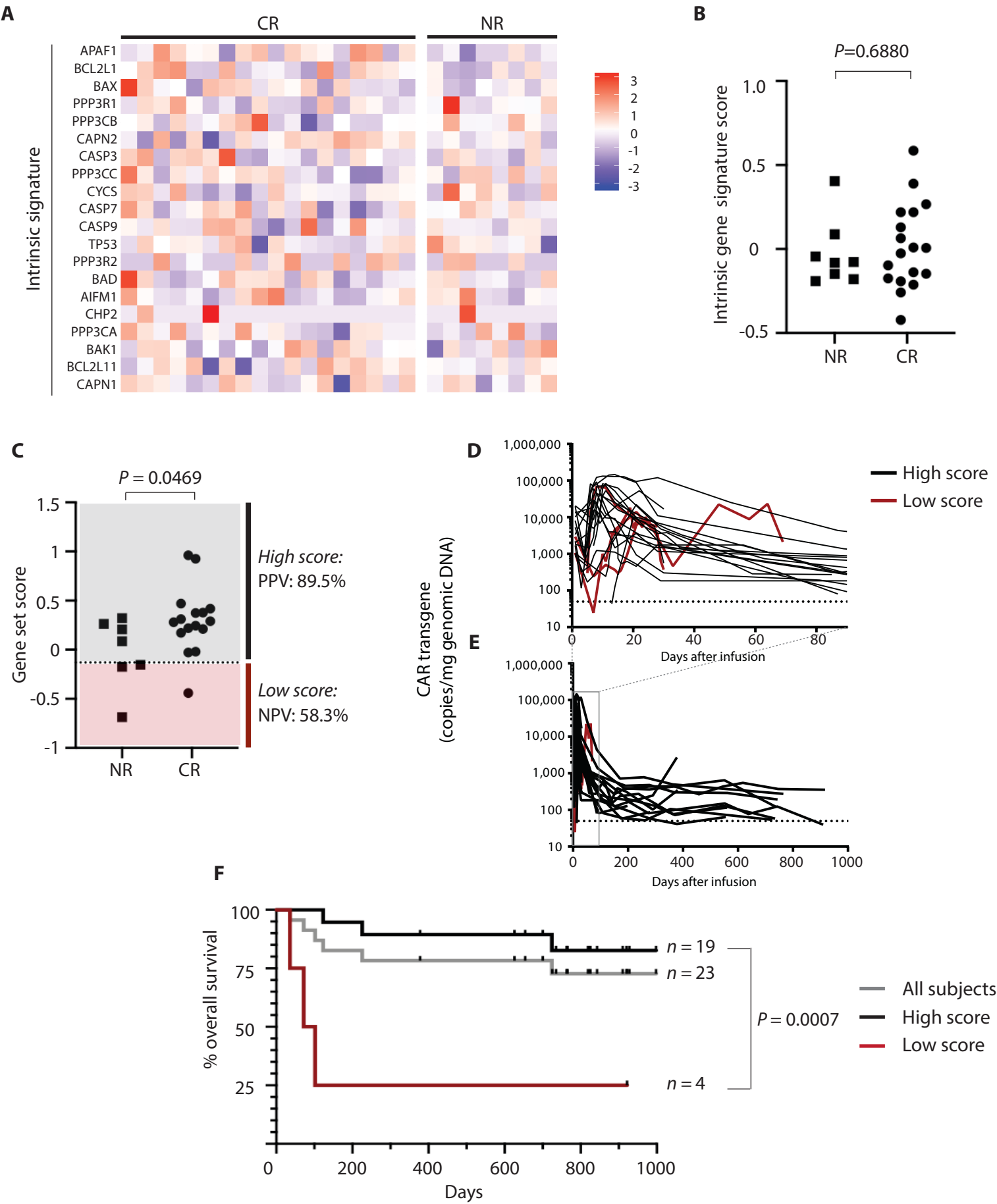


Supplementary Figure 7



**Figure S7. Death receptor gene expression is associated with clinical outcomes.**

(A) RNA expression heatmap of intrinsic pathway pro-apoptotic genes (“intrinsic gene signature”) from pre-treatment bone marrow samples.

(B) Integrated gene set score of intrinsic apoptotic signatures in patients with durable complete remissions (CR) and non-responders (NR).

(C) Death receptor signature score adjusted for marrow blast counts prior to treatment in CRs and NRs.

(D-E) Pharmacokinetic analysis of tisagenlecleucel in patient peripheral blood over the first (D) 90 and (E) 1000 days after infusion, as measured by qPCR of CAR transcripts grouped by marrow blast count-adjusted gene set score.

(F) Overall survival of all patients analyzed, grouped by adjusted death receptor signature score.

\*P<0.05, \*\*P<0.01, \*\*\*P<0.001, \*\*\*\*P<0.0001, ns: not significant